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| APPLICATION NO. | FILING DATE | FIRST NAMED INVENTOR | ATTORNEY DOCKET NO. | CONFIRMATION NO. |
|-----------------|-------------|----------------------|---------------------|------------------|
| 09/825,682 | 04/04/2001 | Elena Feinstein | 65503-B/JPW/MS | 3555 |

7590

04/27/2005

John P. White
Cooper & Dunham LLP
1185 Avenue Of the Americas
New York, NY 10036

EXAMINER

JOHANNSEN, DIANA B

ART UNIT

PAPER NUMBER

1634

DATE MAILED: 04/27/2005

Please find below and/or attached an Office communication concerning this application or proceeding.

SUPPLEMENTAL EXAMINER'S AMENDMENT

1. An examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it **MUST** be submitted no later than the payment of the issue fee.

2. **Amend the specification as follows:**

Amend the specification as specified in the attached Amendment, which was requested by the examiner on March 2, 2005, and submitted to the examiner by facsimile on April 11, 2005.

3. It is noted that certain portions of the Amendment submitted April 11, 2005 are not in the format specified in MPEP 1302.04 for facsimile attachments to an examiner's amendment (specifically, 3 paragraphs provided by applicant are in a "marked-up" format, rather than a "clean" format). Accordingly, in the event that the "marked-up" versions are unusable for printing purposes, "clean" versions of the paragraphs submitted by Applicant are set forth below:

On page 55, lines 15 to 26:

--Many of the unexpected phenomena can indicate the limitation of previous understanding, and serve as a starting point for class definition. However, "outlying" hybridizations can also indicate quality problems. Overall, in each set (Figures 1-4) most of the separation between hybridizations is consistent with the expected TCC and normal urothelium separation. Even in hybridizations of lower quality, such as those of the second set, a clear separation between TCC and normal samples is observed.—

On page 55, lines 29 to 39:

--One of the TCC samples in the first set (TC6) is such an "outlier" (Figure 1), as well as one of the normal samples in the second set, and another normal sample (TC35) in the third. (The "outliers" do not appear to be misclassifications). For example, TC35 (a normal sample which is an "outlier" in the third set) does not behave like a TCC sample. Rather those genes that are up-regulated in TCC samples are down-regulated in TC35).—

On page 59, lines 1 to 13:

--None of the "outliers" was eliminated from subsequent analysis steps. Rather, they were included to facilitate the selection of a more robust marker set (Figures 1-4). Here, more complex relations are observed between global expression profiles. First, the two invasive hybridizations (TC34 and TC45), are distinct from other TCC samples (Figures 1-6). Second, the relationship between global Ta and T1 profiles is not straightforward.

Art Unit: 1634

Most of the Ta samples form a unique cluster in the 3rd set, while the T1 samples are more dispersed.—

4. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Diana B. Johannsen whose telephone number is 571/272-0744. The examiner can normally be reached on Monday-Friday, 7:30 am-4:00 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, W. Gary Jones can be reached at 571/272-0745. The fax phone number for the organization where this application or proceeding is assigned is 703-872-9306.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free).



Diana B. Johannsen
Primary Examiner
Art Unit 1634
April 13, 2005

Attachment to the Supplemental Examiner's Amendment

Apr-11-05 06:59pm From-Cooper&Dunham LLP

+212 391 0526

T-398 P.001

F-408

Requested
mmj/os
4/13/05

COOPER & DUNHAM LLP

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DOCKET: 2094/65503-B U.S. SERIAL NUMBER: 09/825,682

MESSAGE: AMENDMENT AFTER PAYMENT OF ISSUE FEE IN RESPONSE TO MARCH 2, 2005 TELEPHONE REQUEST BY EXAMINER JOHANNSEN

=====

THE INFORMATION CONTAINED IN THIS FACSIMILE TRANSMISSION IS INTENDED SOLELY FOR THE PERSONAL AND CONFIDENTIAL USE OF THE DESIGNATED RECIPIENT(S) NAMED ABOVE. THIS TRANSMISSION MAY BE AN ATTORNEY-CLIENT COMMUNICATION CONTAINING INFORMATION THAT IS PRIVILEGED AND CONFIDENTIAL. IF THE READER OF THIS MESSAGE IS NOT A DESIGNATED RECIPIENT OR AN AGENT RESPONSIBLE FOR DELIVERING IT TO A DESIGNATED RECIPIENT, YOU ARE HEREBY NOTIFIED THAT YOU HAVE RECEIVED THIS DOCUMENT IN ERROR, AND THAT ANY REVIEW, DISTRIBUTION, OR COPYING OF THIS MESSAGE IS STRICTLY PROHIBITED. IF YOU HAVE RECEIVED THIS COMMUNICATION IN ERROR, OR IF UPON READING THIS DOCUMENT YOU HAVE REASON TO BELIEVE THAT THE DOCUMENT WAS INADVERTENTLY SENT TO YOU, PLEASE NOTIFY US IMMEDIATELY BY COLLECT TELEPHONE CALL AND RETURN THE ORIGINAL MESSAGE TO US BY MAIL. THANK YOU.

Docket. No. 65503-B/JPW/DNS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Elena Feinstein and Orna Mor
Serial No.: 09/825,682 Group Art Unit: 1634
Filed : April 4, 2001 Examiner: D. Johannsen
For : METHODS OF DIAGNOSING BLADDER CANCER

1185 Avenue of the Americas
New York, New York 10036
April 11, 2005

BY FACSIMILE - (571)273-0744

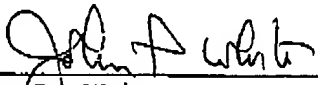
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FACSIMILE CERTIFICATION OF TRANSMISSION
IN CONNECTION WITH THE ABOVE-IDENTIFIED APPLICATION

Date of Facsimile: April 11, 2005. I hereby certify that this paper including Amendment After Payment of Issue Fee in Response to March 2, 2005 Telephone Request By Examiner Johannsen is being transmitted to the U.S. Patent and Trademark Office on the date indicated above by facsimile and is addressed to U.S. Patent and Trademark Office, P.O. Box 1450, Alexandria, VA 22313-1450 Attn: D. Johannsen.

Printed Name: Daniel Smith

Respectfully submitted,


John P. White
Registration No. 28,678
Attorney for Applicants
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1185 Avenue of the Americas
New York, New York 10036
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Docket No. 65503-B/JPW/DNS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicants: Elena Feinstein and Orna Mor
Serial No.: 09/825,682 Examiner: D. Johannsen
Filed : April 4, 2001 Group Art Unit: 1634
For : METHODS OF DIAGNOSING OF BLADDER CANCER

1185 Avenue of the Americas
New York, New York 10036
April 11, 2005

BY FACSIMILE - (571)-273-0744

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

Sir:

**AMENDMENT AFTER PAYMENT OF ISSUE FEE IN RESPONSE TO MARCH 2,
2005 TELEPHONE REQUEST BY EXAMINER JOHANNSEN**

This Amendment is submitted in response to a March 2, 2005 telephone request from Examiner Johannsen, communicated to Daniel N. Smith of the undersigned's office during which Examiner Johannsen requested amendments to the specification of the above-identified application. Accordingly, applicants submit this Amendment in response to the Examiner's request.

Amendments to the Specification begin on page 2 of this paper.

Remarks/Arguments begin on page 32 of this paper.

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Serial No.: 09/825,682
Filed: April 4, 2001
Page 2

Amendments to the Specification

Please add the following section on page 8, line 5 of the specification immediately before the beginning of "DETAILED DESCRIPTION OF THE INVENTION":

-- BRIEF DESCRIPTION OF THE FIGURES

Figure 1: This figure shows relationships between hybridizations' hierarchical clustering of Set #1 hybridizations. Either the Pearson correlation coefficient or a standard Euclidean distance was used as the distance measure between differential hybridization vectors. Hybridizations were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.

Figure 2: This figure shows relationships between hybridizations' hierarchical clustering of Set #2 hybridizations. Either the Pearson correlation coefficient or a standard Euclidean distance was used as the distance measure between differential hybridization vectors. Hybridizations were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.

Figure 3: This figure shows relationships between hybridizations' hierarchical clustering of Set #3 hybridizations. The figure is a tree diagram for 21 variables with unweighted pair-group average. The Pearson correlation coefficient was used as the distance measure between differential hybridization vectors. Hybridizations

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were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.

Figure 4: This figure shows relationships between hybridizations' hierarchical clustering of Set #3 hybridizations. The figure is a tree diagram for 21 variables with unweighted pair-group average. The standard Euclidean distance was used as the distance measure between differential hybridization vectors. Hybridizations were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.

Figure 5: This figure shows relationships between hybridizations' hierarchical clustering for all TCC sample hybridizations. The figure includes raw data with unweighted pair-group average. The Pearson correlation coefficient was used as the distance measure between differential hybridization vectors. Hybridizations were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.

Figure 6: This figure shows relationships between hybridizations' hierarchical clustering for all TCC sample hybridizations. The figure includes raw data with unweighted pair-group average. The standard Euclidean distance was used as the distance measure between

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differential hybridization vectors. Hybridizations were clustered according to these distances by average linkage hierarchical clustering. Missing values were deleted on a case-wise basis. Clusters of Missing values hybridizations can be identified and evaluated in light of existing knowledge.--

Please amend the paragraph on page 55, lines 15 to 26 of the specification as follows:

--Many of the unexpected phenomena can indicate the limitation of previous understanding, and serve as a starting point for class definition. However, "outlying" hybridizations can also indicate quality problems. Overall, in each set ~~(Table B3)~~ (Figures 1-4) most of the separation between hybridizations is consistent with the expected TCC and normal urothelium separation. Even in hybridizations of lower quality, such as those of the second set, a clear separation between TCC and normal samples is observed.--

Please amend the paragraph beginning on page 55, lines 29 to 39 of the specification as follows:

--One of the TCC samples in the first set (TC6) is such an "outlier" ~~(Table B3)~~ (Figure 1), as well as one of the normal samples in the second set, and another normal sample (TC35) in the third. (The "outliers" do not appear to be misclassifications). For example, TC35 (a normal sample which is an "outlier" in the third set) does not behave like a TCC sample. Rather those genes that are up-regulated in TCC samples are down-regulated in TC35).--

Please delete pages 56 to 58 of the specification.

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Serial No.: 09/825,682
Filed: April 4, 2001
Page 5

Please amend the paragraph beginning on page 59, lines 1 to 13 of the specification as follows:

-- None of the "outliers" was eliminated from subsequent analysis steps. Rather, they were included to facilitate the selection of a more robust marker set ~~(Table B3)~~ (Figures 1-4). Here, more complex relations are observed between global expression profiles. First, the two invasive hybridizations (TC34 and TC45), are distinct from other TCC samples ~~(Tables B3 and B4)~~ (Figures 1-6). Second, the relationship between global Ta and T1 profiles is not straightforward. Most of the Ta samples form a unique cluster in the 3rd set, while the T1 samples are more dispersed.--

Please renumber pages 59 to 82 of the specification as pages 56 to 79.

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 Page 6

Please replace the existing Table E on pages 83 and 84 of the specification with the following new Table E expanded into 8 pages to improve legibility:

TABLE E (Page 1)

| Index | GeneDescription1 |
|-------|--|
| 1 | Huron 54 kDa protein mRNA, complete cds; nt non genomic(centrality) REPEAT; contig. ICC_2966, RF: to |
| 2 | none; 11, ICC_7403, 1, M13F; to none; 25, ICC_7403, 1, M13R; to |
| | (AL121586) d47704.1 (novel protein similar to otoferlin and dysferlin) (Homo sapiens) ; nt(centrality); 10, ICC_70E2, 1, M13F; to Homo sapiens serine protease inhibitor, Kunitz type, 2 (SPIN12), mRNA; nt non genomic(centrality); 24, ICC_70E2, 1, M13R; to |
| 3 | Homo sapiens full length insert cDNA clone ZC48G12; nt non genomic(centrality); contig. ICC_7587, RF: to |
| 4 | Homo sapiens GFI-anchored metastasis-associated protein homolog (C4.4A), mRNA; nt non genomic(centrality); contig. ICC_89H5, RF: to |
| 5 | Homo sapiens cDNA: FLJ22720, clone HSI14320 nt non genomic(centrality); 16, ICC_101D4, 1, M13F; to ANKRD21 protein (Homo sapiens) 300, 1 (AB037360) ANKRD21 (Homo sapiens) ; nt(centrality); 30, ICC_101D4, 1, M13R; to |
| 6 | low molecular mass ubiquitinone-binding protein (Homo sapiens) UCRA_HUMAN UBIQUINOL-CYTOCHROME C REDUC; nt(centrality); contig. ICC_67C11, RF: to |
| 7 | none; 14, ICC_7981, 1, M13F; to Homo sapiens quiescin Q6 (GSCN6), mRNA; nt non genomic(centrality); 28, ICC_7981, 1, M13R; to |
| 8 | Homo sapiens mRNA: cDNA DKF7D564C2282 (from clone DKF7D564C2282); nt non genomic(centrality); contig. ICC_74H12, RF: to |
| 9 | Homo sapiens full length insert cDNA clone ZC48G12; nt non genomic(centrality); contig. ICC_56G1, RF: to |
| 10 | NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 2 (14.5kD, 81.45b) (Homo sapiens) N48M_HUMAN; nt(centrality); contig. ICC_60B2, RF: to |
| 11 | |
| 12 | |
| 13 | |
| 14 | |

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TABLE E (Page 2)

| Accel | GeneID | TC7A_BDE_DIFF | TC8A_BDE_DIFF | TC9A_BDE_DIFF | TC10A_BDE_DIFF |
|-------------------------------------|------------|---------------|---------------|---------------|----------------|
| gi 407307 gb U02493.1 HSU02493 | ICC-29E_6 | -1 | -1.2 | 1.1 | 1 |
| | ICC-74D_3 | -1.1 | -1 | 1.2 | -1.1 |
| gi 7671662 emb CA889410.1 | ICC-7DE_2 | -1.2 | 1.1 | 1.2 | -1.1 |
| gi 10863908 ref NM_021102.1 | ICC-75B_7 | -1.1 | 1 | 1.2 | -1.2 |
| gi 3483555 gb AF086210.1 HUMZC48G12 | | | | | |
| gi 7666943 ref NM_014400.1 | ICC-89H_5 | -1.1 | -1 | 1.1 | 1 |
| gi 10439219 dbj AK026373.1 AK026373 | ICC-101D_4 | -1.1 | -1.1 | 1.1 | -1.1 |
| gi 7705278 ref NP_057460.1 | | | | | |
| gi 7667486 ref NP_055217.1 | ICC-67C_11 | 1 | -1.1 | -1 | 1 |
| gi 4506360 ref NM_002826.1 | ICC-79B_1 | -1.1 | 1 | 1.2 | -1.1 |
| gi 7328021 emb AL161966.1 HSM802543 | ICC-74H_12 | -1.1 | -1.1 | 1.3 | -1.1 |
| gi 3483555 gb AF086210.1 HUMZC48G12 | ICC-56G_1 | -1 | -1 | 1.3 | -1.1 |
| | ICC-47D_9 | 1.1 1+ | | -1 | -1.1 |
| gi 4768784 ref NP_004540.1 | ICC-40B_2 | -1.1 | | -1.1 | -1.1 |
| | ICC-23D_4 | 1.1 | -1.4 | -1.2 | 1.2 |
| | ICC-20F_5 | -1.2 | 1.1 | 1.2 | -1.2 |

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TABLE B (Page 3)

| TC11A_BDE_DIFF | TC22A_BDE_DIFF | TC21A_BDE_DIFF | TC23A_BDE_DIFF | TC24A_BDE_DIFF | TC47A_BDE_DIFF | TC36A_BDE_DIFF |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| 1.2 | -1.1 | 1.3 | -1.2 | 1.1 | -1.2 | 1.1 |
| -1 | 1.1 | 1 | 1 | 1.1 | -1.2 | 1.1 |
| -1.1 | 1.2 | 1.1 | 1 | 1 | -1.4 | 1.2 |
| -1 | 1.1 | -1 | 1 | 1 | -1.2 | 1.1 |
| -1 | 1.2 | -1 | 1.1 | 1.1 | -1.2 | 1.1 |
| 1.2 | 1.1 | 1.1 | 1.1 | 1.1 | -1.3 | 1.1 |
| 1.1 | 1.1 | 1.1 | -1 | -1.2 | -1.2 | -1 |
| -1 | 1.1 | -1 | 1.1 | -1.2 | -1.2 | -1 |
| 1 | 1.2 | 1.2 | -1 | -1.4 | -1.4 | -1.3 |
| -1.1 | 1.2 | 1 | 1 | -1.2 | -1.2 | 1.1 |
| -1 | -1.3 | 1.4 | -1.1 | -1.1 | -1.1 | -1 |
| 1.3 | -1 | 1.2 | -1.1 | 1.1 | 1.1 | -1.2 |
| 1.3 | -1.2 | 1.1 | 1.1 | 1.1 | -1.1 | 1.1 |
| 1.1 | 1.1 | 1 | 1.1 | -1.2 | 1 | -1.2 |

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TABLE 2 (Page 4)

| TC39A_BDE_DIFF | TC46A_BDE_DIFF | TC48A_BDE_DIFF | TC37A_BDE_DIFF | TC35A_BDE_DIFF | TC2A_BDE_DIFF | TC3A_BDE_DIFF |
|----------------|----------------|----------------|----------------|----------------|---------------|---------------|
| -1.1 | 1.1 | 1.4 | -1 | -1.5 | 1.1 | -1.2 |
| 1.3 | 1.3 | 1.1 | -1 | -1.8 | -1.5 | -1.1 |
| 1.3 | 1.3 | 1.2 | -1.1 | -2.1 | -1.3 | -1.5 |
| 1.3 | 1.3 | 1.1 | -1 | -1.9 | -1.2 | 1 |
| 1.3 | 1.3 | 1.1 | -1 | -1.9 | -1.3 | -1.1 |
| 1.2 | 1.3 | 1.1 | -1.1 | -1.7 | -1.2 | -1.1 |
| 1.2 | 1.1 | 1 | -1.2 | -1.2 | -1.4 | 1.1 |
| 1.2 | 1.3 | 1.1 | -1 | -1.8 | -1.2 | -1 |
| 1.3 | 1.3 | 1.2 | -1.1 | -1.6 | -1.2 | -1.3 |
| 1.3 | 1.3 | 1.1 | -1.1 | -1.8 | -1.4 | -1 |
| -1.1 | 1.2 | 1.3 | 1.2 | -1.7 | -1.2 | -1.2 |
| -1.1 | 1.3 | 1.1 | -1.1 | -1.2 | 1 | 1.2 |
| -1 | 1.1 | 1.3 | 1.1 | -1.7 | -1.1 | -1.2 |
| 1.1 | 1.1 | 1.1 | -1 | -1.3 | -1 | 1 |

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TABLE E (Page 5)

| TC6A_BDE_DIFF | TC6A_BDE_DIFF | TC8A_BDE_DIFF | TC16A_BDE_DIFF | TC17A_BDE_DIFF | TC18A_BDE_DIFF | TC26A_BDE_DIFF |
|---------------|---------------|---------------|----------------|----------------|----------------|----------------|
| 14 | 12 | -1.1 | -1 | -1.5 | -1 | 14.4 |
| 1 | 1.5 | 1.1 | 1 | 1.3 | 1.5 | 1.5 |
| | | | | | | |
| -1.3 | 1.3 | -1 | 1.2 | 1.5 | 1.3 | 1.4 |
| -1.4 | 1.3 | 1.3 | 1.1 | 1.4 | 1.3 | 1.5 |
| | | | | | | |
| -1.3 | 1.2 | 1 | 1.1 | 1.5 | 1.1 | 1.5 |
| | | | | | | |
| -1.5 | -1 | -1 | 1 | 1.4 | 1.7 | 1.5 |
| | | | | | | |
| 1.1 | -1 | -1 | 1.1 | 1.5 | 1.5 | 1.5 |
| | | | | | | |
| 1.1 | -1.2 | 1 | 1 | 1.4 | 1.4 | 1.5 |
| | | | | | | |
| -1.1 | 1.1 | -1.2 | 1.1 | 1.4 | 1.4 | 1.5 |
| -1.4 | 1.3 | 1.2 | 1.1 | 1.4 | 1.5 | 1.5 |
| -1.6 | 1.2 | -1 | 1.1 | -1.3 | 1 | 1.3 |
| | | | | | | |
| -1.2 | 1 | 1 | 1.4 | 1.2 | 1.3 | 1.5 |
| -2 | 1.4 | 1.1 | -1.4 | -1.5 | -1.3 | 1.2 |
| -1.2 | -1.1 | -1.1 | -1.2 | 1.2 | 1.4 | 1.3 |

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TABLE E (Page 6)

| TC19A_BDE_DIFF | TC20A_BDE_DIFF | TC32A_BDE_DIFF | TC33A_BDE_DIFF | TC41A_BDE_DIFF | TC42A_BDE_DIFF | TC44A_BDE_DIFF |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| 1.1 | 1.4 | -1.4 | -1.1 | -1.1 | -1.3 | -1.3 |
| 1.1 | 1.3 | -1.2 | 1.1 | 1.1 | 1.1 | 1.2 |
| 1.2 | 1.3 | -1.3 | -1.2 | 1.2 | -1 | 1.2 |
| 1.4 | 1.1 | -1.1 | -1 | 1.1 | 1.1 | 1.1 |
| 1.4 | 1.1 | -1.1 | -1 | 1.1 | 1.1 | -1.1 |
| 1.2 | 1.3 | -1.3 | -1.2 | 1.1 | -1.1 | -1 |
| 1.4 | 1.4 | -1.3 | -1.3 | 1.1 | -1 | -1 |
| 1.4 | 1.1 | -1.1 | 1 | 1.1 | -1 | 1.1 |
| 1.2 | 1.4 | -1.5 | -1.4 | 1.1 | -1.1 | 1.2 |
| 1.4 | 1.3 | -1.1 | 1 | 1.2 | 1 | 1.1 |
| 1.3 | 1.2 | -1.5 | -1.2 | -1.2 | -1.3 | -1.3 |
| 1.2 | 1.2 | -1.3 | -1.2 | -1.1 | -1.4 | -1.2 |
| -1 | -1.1 | -1 | -1.1 | 1 | -1.3 | -1.1 |
| 1.4 | 1.1 | -1.2 | -1.5 | -1 | -1.2 | -1.3 |

Applicants: Elena Feinstein and Orna Mor
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TABLE B (Page 7)

| TC31A_BDE_DIFF | TC39A_BDE_DIFF | TC43A_BDE_DIFF | TC40A_BDE_DIFF | TC30A_BDE_DIFF | TC28A_BDE_DIFF | TC29A_BDE_DIFF |
|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| -1.1 | -1.2 | -1.3 | -1.3 | -1.3 | -1.3 | 1.2 |
| -1.3 | -1.1 | -1.4 | -1.2 | -1.2 | -1.1 | 1.2 |
| -1.3 | -1.1 | -1.4 | -1.2 | -1.2 | -1.1 | 1.1 |
| -1.3 | -1.1 | -1.5 | -1.3 | -1.3 | -1.1 | 1.1 |
| -1.2 | -1.2 | -1.5 | -1.2 | -1.1 | -1.1 | 1.1 |
| -1.3 | -1.2 | -1.4 | -1.4 | -1.1 | -1.3 | -1.1 |
| -1.4 | -1.2 | -1.4 | -1.5 | -1.4 | -1.1 | -1.1 |
| -1.1 | -1.1 | -1.4 | -1.3 | -1.1 | -1.1 | 1.2 |
| -1.3 | -1.2 | -1.5 | -1.4 | -1.4 | -1.1 | 1 |
| -1.3 | -1.1 | -1.5 | -1.3 | -1.3 | -1.1 | 1.1 |
| -1 | -1.4 | -1.5 | -1.4 | -1.5 | -1.1 | 1.2 |
| -1.2 | -1.8 | -1.4 | -1.3 | -1.3 | -1.1 | -1.2 |
| 1.2 | -1.3 | 1 | -1.1 | -1.2 | 1.4 | 1.4 |
| -1.3 | 1 | -1.2 | -1 | -1.3 | 1.1 | -1.2 |

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| TC34A_BDE_DIFF | TC45A_BDE_DIFF |
|----------------|----------------|
| 1.1 | 1.1 |
| 1.4 | 1.1 |
| 1.3 | 1.2 |
| 1.2 | 1.1 |
| 1.2 | 1 |
| 1.1 | 1.1 |
| -1.1 | -1 |
| 1.4 | 1.1 |
| 1 | 1.3 |
| 1.3 | 1 |
| 1.1 | -1.1 |
| 1.2 | 1.1 |
| 1.3 | -1.1 |
| -1.2 | 1.2 |

TABLE E (Page 8)

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Please replace the existing Table 1 on pages 85 and 86 of the specification with the following new Table 1 expanded into 8 pages to improve legibility:

TABLE 1 (Page 1)

| Gene/Description and clone ID |
|---|
| 1 Homo sapiens keratin 19 (KRT19) gene, complete cd : nt_non_genomic(Identity):47_TCC_91811_M13F.TXT1a |
| 2 Human 40-kDa keratin intermediate filament precursor : nt_non_genomic(Identity):20_TCC_60H4_M13F.TXT1a |
| 3 Human mRNA fragment for mesothelial type II kerat : nt_non_genomic(Identity):04_TCC_94G3_M13F.TXT1a |
| 4 Homo sapiens cystatin B (CSTB) gene, promoter reg : nt_non_genomic(Identity):30_TCC_76B3_M13F_F04_042.ab1.TXT |
| 5 Homo sapiens S100 calcium-binding protein P (S100P) : nt_non_genomic(Identity):29_TCC_48G1_M13F.TXT1a |
| 6 Homo sapiens syndecan 1 (SDC1) mRNA : nt_non_genomic(Identity):26_TCC_75E3_M13F_B04_082.ab1.TXT |
| 7 Homo sapiens S100 calcium-binding protein A13 (S10) : nt_non_genomic(Identity):28_TCC_44C1_M13F.TXT1a |
| 8 Homo sapiens mRNA for hepatocyte growth factor ac : nt_non_genomic(Identity):35_TCC_21D8_M13F_C05_067.ab1.a |
| 9 Homo sapiens midline (neurotrophin growth-promoting fac : nt_non_genomic(Identity):82_TCC_89G3_M13F_B11_092.ab1.TXT |
| 10 Homo sapiens soluble carrier family 2 (fractilated) : nt_non_genomic(Identity):37_TCC_57B3_M13F.TXT |
| 11 Homo sapiens S100 calcium-binding protein A11 (cal : nt_non_genomic(Identity):31_TCC_65B9_M13F.TXT1a |
| 12 Homo sapiens fatty acid binding protein 5 (fsovias : nt_non_genomic(Identity):11_TCC_25F2_M13F.TXT |
| 13 Homo sapiens Opa-interacting protein OIP3 mRNA, p : nt_non_genomic(Identity):38_TCC_56E11_M13F.TXT |
| 14 Homo sapiens glutamyl-PRNA synthetase (GARS), en : nt_non_genomic(Identity):46_TCC_78B11_M13F_F06_058.ab1.TXT |
| 15 Homo sapiens anterior gradient 2 (Xenopus laevis) : nt_non_genomic(Identity):25_TCC_50G5_M13F.TXT |
| 16 Homo sapiens myristoylated alanine-rich protein k : nt_non_genomic(Identity):10_TCC_53H11_T9 |
| 17 Homo sapiens leukemia-associated phosphoprotein p1 : nt_non_genomic(Identity):46_TCC_27H5_M13F_F08_058.ab1.a |
| 18 Homo sapiens type II membrane serine protease (LO : nt_non_genomic(Identity):53_TCC_79G2_M13_FEO7_054.ab1.TXT |
| 19 Homo sapiens putative secreted protein XAG mRNA, c : nt_non_genomic(Identity):26_TCC_50G8_M13F.TXT |
| 20 H sapiens (xscad) mRNA, 340bp : nt_non_genomic(Identity):40_TCC_19F11_M13F1a |

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TABLE 1 (Page 2)

| Accession | GeneID | G2/3 | | G2/3 | |
|-----------------------------------|------------|------|---------------|------|---------------|
| | | T1 | TC2A BDE DIFF | T1 | TC3A BDE DIFF |
| gi16728680 gb AF202321.1 AF202321 | TCC-91B_11 | 3.7 | | 3 | 5.4 |
| gi1184658 gb J03607.1 HUMIFP | TCC-60H_4 | 3.7 | | 2.7 | 5.9 |
| gi134067 emb X03212.1 HSEK7R | TCC-94G_3 | 3.3 | | 2.7 | 6.3 |
| gi1726301 gb AF208234.1 AF208234 | TCC-76B_3 | 5.7 | | 2.2 | 3 |
| gi15174662 ref NM_005980.1 | TCC-48G_1 | 2.7 | | 4.8 | 8.9 |
| gi14506858 ref NM_002897.1 | TCC-75E_3 | 1.9 | | 2.6 | 2.5 |
| gi15174658 ref NM_005979.1 | TCC-44C_1 | 3.1 | | 4.8 | 9.3 |
| gi12924619 db AB006534.1 AB006534 | TCC-21D_6 | 1.1 | | 1.1 | -2.2 |
| gi14505134 ref NM_002391.1 | TCC-89G_3 | 2.2 | | 1.7 | 3.7 |
| gi15730050 ref NM_006616.1 | TCC-57B_3 | 4.8 | | 1.2 | 2.2 |
| gi15032056 ref NM_005820.1 | TCC-65B_9 | 3.5 | | 2 | 3.4 |
| gi14557580 ref NM_001444.1 | TCC-25F_2 | 2.1 | | 2.3 | 1.1 |
| gi12815805 gb AF025439.1 AF025439 | TCC-56E_11 | 3.4 | | 2.1 | 2.4 |
| gi14826959 ref NM_005051.1 | TCC-78B_11 | 2.2 | | 2.8 | 5.3 |
| gi15453540 ref NM_008408.1 | TCC-50G_5 | 2.4 | | 5.6 | 3.4 |
| gi14505062 ref NM_002356.1 | TCC-53H_11 | 1.8 | | 1 | -1.6 |
| gi15031850 ref NM_005563.1 | TCC-27H_5 | 1.8 | | 1.7 | 2 |
| gi17705976 ref NM_016425.1 | TCC-79G_2 | 5.6 | | 2.6 | 7.2 |
| gi16652811 gb AF088867.1 AF088867 | TCC-50G_6 | 2.3 | | 5.7 | 3.6 |
| gi1533986 emb Z36852.1 HSXSCAD | TCC-13F_11 | -1.2 | | -1.1 | -2 |

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TABLE 1 (Page 3)

| G2/3 | G1/2 | normal | normal | normal | normal | normal |
|---------------|---------------|---------------|---------------|---------------|----------------|----------------|
| T1 | T1 | TC6A_BDE_DIFF | TC7A_BDE_DIFF | TC8A_BDE_DIFF | TC9A_BDE_DIFF | TC10A_BDE_DIFF |
| TC5A_BDE_DIFF | TC6A_BDE_DIFF | TC7A_BDE_DIFF | TC8A_BDE_DIFF | TC9A_BDE_DIFF | TC10A_BDE_DIFF | TC11A |
| 1.5 | 3.1 | 1 | -2.5 | -2 | 1.2 | -1.2 |
| 1.5 | 2.9 | 1 | -2.6 | -1.9 | 1.3 | -1.1 |
| 0.1 | 1.6 | 1 | -2.1 | -1.8 | 1.3 | -1.4 |
| 1.6 | 1.3 | 1 | -2 | -1.8 | -1 | -1.2 |
| 1.7 | 1.7 | 1 | -2.6 | -2.5 | 2.1 | 1.6 |
| 1 | 1.6 | 1 | -1.7 | -1.3 | -1.1 | -1.5 |
| 1.8 | 1.6 | 1 | -2.6 | -2.4 | 1.9 | 1.4 |
| 2 | 1.8 | 1 | -1.6 | -1.2 | 1.1 | -1.5 |
| -1.5 | 1.9 | 1 | -1.2 | 1.2 | -1.8 | -1.2 |
| 1.2 | 3.2 | 1 | -2.1 | -1.5 | 1.1 | -1.6 |
| 1.5 | 1.6 | 1 | -1.4 | -1.7 | 1.1 | -1.1 |
| 2.6 | 5 | 1 | -1.5 | -1.5 | 2 | 1 |
| 1.1 | 1.6 | 1 | -1.1 | -1.1 | -1.3 | 1.1 |
| 1.6 | 1.6 | 1 | -1.1 | -1.3 | 1.1 | 1.1 |
| -1.2 | 1.2 | 1 | -2 | -1.9 | 1.5 | 1.2 |
| 1.6 | 1.7 | 1 | -1.3 | 1.3 | 1.6 | 1.1 |
| 2.2 | 1.6 | 1 | -1.2 | 1.2 | -1.1 | 1.1 |
| -1.6 | -1.2 | 1 | -2.2 | -2.1 | 1.1 | -1.2 |
| -1.1 | 1.3 | 1 | -1.8 | -1.9 | 1.4 | 1.2 |
| 1.8 | 1.8 | 1 | -1.6 | -1.3 | -1 | -1.5 |

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TABLE 1 (Page 4)

| G2 | G2 | High | Low | G3 | Normal |
|----------------|----------------|----------------|----------------|----------------|----------------|
| T1 | Ta | Ta | T1 | T1 | TC21A_BDE_DIFF |
| TC16A_BDE_DIFF | TC17A_BDE_DIFF | TC18A_BDE_DIFF | TC19A_BDE_DIFF | TC20A_BDE_DIFF | |
| 2.6 | 2.4 | 2.5 | 2.6 | 1.7 | -1.3 |
| 2.4 | 2.6 | 3.6 | 2.9 | 1.8 | -1.2 |
| 7.1 | 4.6 | 6.3 | 4.1 | 4.3 | -1.6 |
| 3.6 | 11 | 8.9 | 2.3 | 3.4 | -1.5 |
| 3 | 6.1 | 8.2 | 2.8 | 1.3 | 1.3 |
| 5 | 4.6 | 4 | 2.4 | 4.7 | -1.3 |
| 2.8 | 4.9 | 6.8 | 2.5 | 1.1 | -1.1 |
| 2.7 | 2.6 | 2.6 | 1.7 | 2 | 1.2 |
| 1.9 | 2.5 | 1.9 | 1.4 | 2.9 | 1.1 |
| 2.7 | 1.8 | 2.9 | -1 | 1.4 | -1.2 |
| 2.9 | 3.8 | 2.7 | 2.3 | 1.5 | -1.8 |
| 1.2 | 1.7 | 4.6 | 2.2 | 1.6 | -2.5 |
| 2.8 | 3.6 | 4.5 | 2.3 | 1.7 | 1.1 |
| 2.7 | 5 | 2.1 | 1.9 | 1.8 | -1.6 |
| 2.8 | 2.8 | 2.9 | 4.9 | 1.6 | -1.4 |
| 1.9 | 1.6 | 2.5 | 1.5 | 2.2 | -2.1 |
| -1.1 | -1.4 | 1.4 | -1.4 | 1.2 | -1.3 |
| 3.8 | 1.4 | 3.6 | 3.9 | -1.2 | 1.3 |
| 3.1 | 3.7 | 4.5 | 4.4 | 2.1 | -1.3 |
| 1.8 | 2.1 | 2.2 | 1.2 | 1.8 | -1.3 |

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TABLE 1 (Page 5)

| normal | | normal | | normal | | Low | | High | |
|----------------|--|----------------|--|----------------|--|------|------|------|------|
| TC22A_BDE_DIFF | | TC23A_BDE_DIFF | | TC24A_BDE_DIFF | | T1 | G3 | T1 | G3 |
| 1 | | 1.3 | | -2.1 | | 2.6 | 2.4 | 2.2 | 2 |
| 1 | | 1.2 | | -1.9 | | 2.1 | 2.2 | 2 | 1.8 |
| 1 | | 1.8 | | -1.7 | | 4 | 1.5 | 3.5 | 3.6 |
| 1 | | 1.7 | | -1.8 | | 4.4 | -1.3 | 2 | 2.1 |
| 1 | | 1.9 | | -1.1 | | 4.4 | -1.1 | 3.5 | 3.2 |
| 1 | | 1.4 | | -1.1 | | 2.7 | 1.6 | 1.2 | 1.3 |
| 1 | | 1.9 | | -1.1 | | 3.5 | 1.2 | 2.4 | 2 |
| 1 | | 1.5 | | 1.7 | | 2.4 | 3.9 | 2.2 | 1.7 |
| 1 | | 1.4 | | 1 | | 3.7 | 7 | 2 | -1.1 |
| 1 | | 1.2 | | -1.2 | | 2.4 | -1.1 | 2 | 2.7 |
| 1 | | 1.2 | | -2.4 | | 3.8 | -1.1 | 2.4 | 1.1 |
| 1 | | 1.1 | | 1 | | 1.8 | -1.8 | 1 | 5.7 |
| 1 | | 1.4 | | -1.2 | | 3.1 | -1.3 | 1.2 | 1.1 |
| 1 | | 1.2 | | -2 | | 2.4 | 1.1 | 1.7 | 1.3 |
| 1 | | 1.2 | | 1.4 | | 3.1 | -1.3 | 1.8 | 1.2 |
| 1 | | 1.1 | | -2.3 | | 3.9 | -1.3 | 2.5 | 2 |
| 1 | | 1.1 | | 1.6 | | -1.3 | 5.7 | 6.7 | 1.9 |
| 1 | | 2.1 | | 1.4 | | 3.8 | -2.1 | -1.5 | 1.5 |
| 1 | | 1.5 | | 1.2 | | 3.7 | -1.5 | 1.5 | -1 |
| 1 | | -1.1 | | -1.3 | | 1.8 | 4.6 | 2.8 | 1.9 |

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TABLE 1 (Page 6)

| G1/2 | G2 | G2 | INV | normal | normal |
|----------------|----------------|----------------|----------------|----------------|----------------|
| Ta | Ta/T1 | Ta | | | |
| TC31A_BDE_DIFF | TC32A_BDE_DIFF | TC33A_BDE_DIFF | TC34A_BDE_DIFF | TC36A_BDE_DIFF | TC38A_BDE_DIFF |
| 2.1 | 2.3 | 2.4 | -1 | -3.9 | -1.4 |
| 1.8 | 2 | 1.9 | -1.2 | -4.5 | -1.8 |
| 4.3 | 3.2 | 2.1 | 1.1 | -3.3 | -1.2 |
| 1.6 | 4.8 | 2 | 3.3 | -1.4 | -1 |
| 3.7 | 5 | 2.6 | 1.8 | -4 | 1 |
| 4.3 | 3.7 | 2.2 | 1.1 | 1.1 | -1 |
| 2.4 | 3.1 | 1.7 | 1.6 | 1.2 | 1 |
| 2.5 | 2.6 | 2.7 | 2.1 | 2 | -1.3 |
| 2.5 | 1.8 | 2.5 | 1.3 | -1.3 | 1.1 |
| 1.3 | 1.8 | 3.8 | 3 | 1.4 | 1.1 |
| 2.3 | 2.4 | 1.8 | 2.5 | -1.5 | -1.2 |
| 3.5 | 1 | 3.9 | -1.1 | -4.1 | -1.5 |
| 3.1 | 1.6 | 1.8 | -1.1 | 2 | -1.2 |
| -1 | 2 | 1.9 | -1.1 | -2.3 | -1.4 |
| 2.3 | 6.7 | -1.3 | 1.3 | -1.3 | 1.2 |
| 3.7 | 2.6 | 2.5 | -2.1 | -1.2 | 1.1 |
| 1.8 | 1 | 1.7 | 3.5 | 1.5 | 1.3 |
| 5.3 | -1.9 | 3.2 | -1.8 | -1.8 | -1.2 |
| 2.1 | 6 | -1.5 | 1.1 | -1.3 | -1.1 |
| 3 | 3.1 | 3.1 | 2.5 | 2.4 | -1.1 |

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TABLE 1 (Page 7)

| normal | normal | Low | G2/3 | G2 | G2 |
|----------------|----------------|----------------------|----------------------|----------------------|----------------------|
| TC37A_BDE_DIFF | TC38A_BDE_DIFF | Ta TC39A_BDE_DIFF | T1 TC40A_BDE_DIFF | Ta TC41A_BDE_DIFF | Ta TC42A_BDE_DIFF |
| -1.8 | -1.4 | 3.2 | 3.1 | 2.2 | 2.6 |
| -2.3 | -1.6 | 2.9 | 2.5 | 1.8 | 2.4 |
| -1.4 | -1.3 | 3.5 | -1.0 | 2.4 | 2.5 |
| -1.6 | -1 | 4.1 | 2.3 | 1.7 | 1.5 |
| -1.7 | -1.3 | 3.4 | 4.5 | 1.3 | 3.3 |
| -1 | 1 | 2.3 | 3.4 | 2 | 1.9 |
| -1.6 | -1 | 2.4 | 2.7 | 1.1 | 2.4 |
| -1.8 | 1 | 1.4 | 1.6 | 2.6 | 1.6 |
| 1.2 | 1 | 1.8 | 4 | 1.7 | 2.5 |
| 1.4 | 1.1 | 3.8 | 3.4 | 3.2 | 1.4 |
| -1.8 | -1.1 | 2.7 | 1.2 | 2.1 | 1.9 |
| -1.9 | -1.1 | 1.1 | 2.8 | 2.5 | 2 |
| -1.4 | -1 | 2.3 | 2 | 1.8 | 1.9 |
| -1.6 | -1.3 | 1.6 | 2.6 | 1.1 | 1.3 |
| 1.3 | 1.1 | 1.9 | 1.5 | 1.9 | 2.5 |
| -1.2 | 1.1 | 1.3 | 1.6 | 2 | 1.4 |
| 1.2 | 1.1 | 1.9 | 2.5 | 2.4 | 1.7 |
| -1.1 | -1.1 | 2.2 | 1.5 | 2.3 | 2.8 |
| 1 | 1 | 1.6 | 1.2 | 1.9 | 2.3 |
| -1.7 | 1.2 | 1.7 | 1.9 | 2.9 | 2 |

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TABLE 1 (Page 8)

| G2 | T1 | G2 | INV | normal | normal | normal | secreted |
|----------------|----------------|----------------|----------------|----------------|----------------|--------|----------|
| TC43A_BDE_DIFF | TC44A_BDE_DIFF | TC45A_BDE_DIFF | TC46A_BDE_DIFF | TC47A_BDE_DIFF | TC48A_BDE_DIFF | | |
| 1.7 | 3.8 | 1.1 | -1 | 1 | -1.1 | 3.9 | |
| 1.6 | 3.8 | 1.1 | -1.1 | 1 | -1.1 | 3.8 | |
| 1.8 | 5.6 | -1.3 | -1.1 | 1 | -1.2 | 3.8 | |
| 2.2 | 3.3 | 1.2 | 1.1 | 1 | -1.1 | -1.8 | |
| 2.3 | 3.4 | -1.6 | -1.2 | 1 | -1 | -1.2 | |
| 2.2 | 3.1 | 1.1 | -1 | 1 | -1.1 | 1 | |
| 1.5 | 2.9 | -1.4 | 1.1 | 1 | -1 | -1.4 | |
| 2 | 3 | 1.2 | -1.1 | 1 | -1.3 | -2.2 | |
| 1.4 | 2.3 | 1.5 | 1.3 | 1 | 1.1 | -2.6 | |
| 2.6 | 3.8 | 2.7 | 1.1 | 1 | 1 | | |
| 1.2 | 3.1 | 1.3 | 1.1 | 1 | -1.3 | -1.8 | |
| 2.2 | 3.9 | 2.1 | 1.1 | 1 | -1.2 | -1.2 | |
| 1.3 | 2.8 | 1.4 | 1 | 1 | -1.2 | 4.9 | |
| 1.3 | 1.4 | -1.3 | 1.1 | 1 | -1.1 | -1.5 | |
| 1.8 | 2.3 | 1.1 | -1.4 | 1 | -1.2 | | |
| 2 | 1.3 | 1.4 | 1.6 | 1 | -1.1 | 3.8 | |
| 1.4 | 1 | 2.5 | 1 | 1 | 1 | 1.9 | |
| 2.8 | 3.1 | 1.1 | -1.2 | 1 | -1.2 | -1.7 | |
| 1.9 | 2.9 | 1.1 | -1.3 | 1 | -1.1 | -1.4 | |
| 2.1 | 3.2 | 1.3 | 1 | 1 | -1.2 | -2.2 | |

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Please replace the existing Table 2 on pages 87 and 88 of the specification with the following new Table 2 expanded into 10 pages to improve legibility:

TABLE 2 (Page 1)

| | GeneDescription and clone ID |
|----|---|
| 1 | Homo sapiens full length insert cDNA clone ZC48G12; nt non_genomic(identity):03_TCC_57E11_T7.TXT:fa |
| 2 | xq01h07.x1 Soares_NHCCc_cervical_tumor Homo sapien; est(identity):24_TCC_9BC7_M13F.TXT |
| 3 | h68c04.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IM; est(identity):26_TCC_13H10_M13F_B04_032.ab1:fa |
| 4 | none:21_TCC_43E2_M13F.TXT |
| 5 | PC3-BN0053-170200-01-e12 BN0053 Homo sapiens cDNA; est(identity):28_TCC_16D12_M13F_D04_041.ab1:fa |
| 6 | none:08_TCC_70E7_M13F_H01_015.ab1.TXT |
| 7 | Homo sapiens clone RP4-584D14, complete sequence; nt non_genomic(identity):14_TCC_986_M13F_F02_026.ab1:fa |
| 8 | Homo sapiens CG-81 protein (LOC51108), mRNA; nt non_genomic(identity):11_TCC_101E11_M13F.TXT:fa |
| 9 | Homo sapiens mRNA for KIAA0660 protein, complete; nt non_genomic(identity):72_TCC_37E11_M13F_H09_079.ab1:fa |
| 10 | H.sapiens GAINAc-T1 gene, 3UTR; nt non_genomic(identity):54_TCC_30E5_M13F_F07_062.ab1:fa |
| 11 | none:15_TCC_71H8_M13F_G02_019.ab1.TXT |
| 12 | Homo sapiens ETAA16 protein (ETAA16), mRNA; nt non_genomic(identity):09_TCC_101C11_M13F.TXT:fa |
| 13 | Homo sapiens cDNA FL10861 fls, clone NT2RP400157; nt non_genomic(identity):24_TCC_12F3_M13F_H03_031.ab1:fa |
| 14 | h75c10.x1 NCI_CGAP_GU1 Homo sapiens cDNA clone IM; est(identity):59_TCC_34D5_M13F_C08_065.ab1:fa |
| 15 | none:15_TCC_57C3_M13F.TXT:fa |
| 16 | y181a1.1 Soares breast 2NBHBS1 Homo sapiens cDNA; est(identity):29_TCC_17A5_M13F_E04_034.ab1:fa |
| 17 | hypothetical protein C50F7.2 - Caenorhabditis eleg; CONTIG nt(strong):31_TCC_10E8_M13F:fa |
| 18 | none:13_TCC_71E4_M13F_E02_018.ab1.TXT |
| 19 | Homo sapiens mRNA; cDNA DKFZp3410310 (from clone; nt non_genomic(identity):57_TCC_80C9_M13F_A08_058.ab1.TXT |
| 20 | none:44_TCC_70E8_M13F.TXT:fa |

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TABLE 2 (Page 2)

| Accession | GeneID | T1 | TC2A_BDE_DIFF | TC3A_BDE_DIFF |
|-------------------------------------|-------------|-----|---------------|---------------|
| gi 3483555 gb AF086210.1 HUMZC48G12 | TCC-57E_11 | 3.3 | 2.8 | |
| gi 7154678 gb AW516596.1 AW516596 | TCC-96C_7 | 2.8 | 4.3 | |
| gi 7318401 gb AW613215.1 AW613215 | TCC-13H_10 | 2.2 | 1.6 | |
| gi 8257938 gb AW997704.1 AW997704 | TCC-43E_2 | 2.7 | 4.7 | |
| | TCC-16D_12 | 2.7 | 5.3 | |
| | TCC-70E_7 | 3.8 | 2.1 | |
| gi 8468933 gb AC005586.2 AC005586 | TCC-9B_6 | 11 | -1 | |
| gi 7705788 ref NM_016026.1 | TCC-101E_11 | 5.1 | 2.1 | |
| gi 3327133 db AB014560.1 AB014560 | TCC-37E_11 | 8 | -1.5 | |
| gi 2292903 emb Y10343.1 HSY10343 | TCC-30E_5 | 3.3 | 2.3 | |
| | TCC-71H_8 | 1.7 | 1.4 | |
| gi 9506580 ref NM_019002.1 | TCC-101C_11 | 6.1 | 2.2 | |
| gi 7023162 db AK001723.1 AK001723 | TCC-12F_3 | 1.4 | 2 | |
| gi 7318796 gb AW613610.1 AW613610 | TCC-34D_5 | 1.6 | 2.5 | |
| gi 843837 gb F70320.1 F70320 | TCC-57C_3 | 3.5 | 2.8 | |
| gi 7497781 pir T29299 | TCC-17A_5 | 2.7 | 2.6 | |
| | TCC-10E_8 | 1.1 | 1.4 | |
| | TCC-71E_4 | 1.7 | 1.6 | |
| gi 6808331 emb AL137591.1 HSM802346 | TCC-80C_9 | 3.7 | 2 | |
| | TCC-70E_8 | 4.1 | 2.2 | |

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TABLE 2 (Page 3)

| G2/3 | G2/3 | G1/2 | | |
|---------------|---------------|---------------|---------------|---------------|
| T1 | T1 | T1 | normal | normal |
| TC4A_BDE_DIFF | TC5A_BDE_DIFF | TC6A_BDE_DIFF | TC7A_BDE_DIFF | TC8A_BDE_DIFF |
| 3.2 | 1.3 | 2.3 | 1 | -1.3 |
| 5.8 | 5.9 | -1.4 | 1 | -1.3 |
| 2.1 | 1 | 1.2 | 1 | -1.4 |
| 7.3 | 1.5 | 1.7 | 1 | 2.3 |
| 2.4 | 8.8 | -1.4 | 1 | 2.7 |
| 3.6 | 1.6 | 1.5 | 1 | -1.6 |
| 3.9 | 4.1 | -1.6 | 1 | -1.6 |
| 3.1 | 1.6 | 1.3 | 1 | -1.5 |
| 3.1 | 3.1 | -1.3 | 1 | -1 |
| -1.2 | 1.3 | 2 | 1 | 1.5 |
| -1 | 2.5 | 2 | 1 | -1.5 |
| 3.2 | 1.9 | 1.2 | 1 | -2.3 |
| 1.1 | -1.3 | 1.6 | 1 | -1 |
| 1.9 | 1.1 | 1.4 | 1 | 1.1 |
| 2.9 | 1.2 | 2.3 | 1 | -1.1 |
| 1.9 | 1.7 | 9.3 | 1 | 1.2 |
| 1.6 | 1.5 | -1.1 | 1 | 1.3 |
| 1.3 | 2.3 | 2.1 | 1 | -1.4 |
| 3.2 | 1.7 | 1.3 | 1 | -1.5 |
| 3.7 | 1.7 | 1.5 | 1 | 1.3 |

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TABLE 2 (Page 4)

| normal | normal | normal | G2 | G2 | High |
|---------------|----------------|--------|----------------|----------------|----------------|
| TC9A BDE DIFF | TC10A BDE DIFF | TC11A | T1 | Ta | Ta |
| -1.5 | 1.2 | -1.2 | TC16A BDE DIFF | TC17A BDE DIFF | TC18A BDE DIFF |
| -1 | 2.7 | 1.2 | 2.2 | 2.6 | 3.7 |
| 1.1 | 1 | -1 | 4 | 7.5 | 2.2 |
| -2.3 | 2.1 | 1.7 | 1.3 | 1.2 | 1.3 |
| 1.3 | 1.3 | -1.2 | 1.8 | 5.1 | 6.2 |
| -2.1 | 1.1 | -1.1 | 3.6 | 4.4 | -1.1 |
| 1 | -1.2 | -1.4 | 3.5 | 4.8 | 2.9 |
| -1.4 | 1.1 | 1.2 | 3 | 3.7 | 1.3 |
| -1.2 | -1.4 | -1.6 | 2.8 | 7.2 | 4.4 |
| 1.1 | 1.8 | 2.1 | 1.6 | 2 | -1 |
| -1.2 | 1.1 | -1.3 | -1.1 | 1.7 | 1.7 |
| -1.4 | -1 | 1 | 2.1 | 2.6 | 3 |
| 1.1 | 2 | 1.2 | 2.6 | 6.8 | 4.2 |
| 1.1 | 1.9 | 1.4 | 1.2 | 1.7 | 1.5 |
| -1.6 | 1.2 | 1.2 | -1.7 | -1.2 | -1.1 |
| 1.5 | 1.8 | 1.6 | 1.6 | 2.6 | 2.9 |
| 1.3 | 1 | -1.1 | 1.5 | -1 | 1.4 |
| -1.3 | 1 | -1.1 | -1.1 | -1.7 | -1.7 |
| -1.3 | 1.1 | -1.3 | 1.8 | 2.3 | 2.7 |
| -1.7 | 1.1 | -1 | 1.1 | 1.8 | 1.9 |
| | | | 2.9 | 4.3 | 2.4 |

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TABLE 2 (Page 5)

| Low | CG3 | T1 | normal | normal | normal |
|----------------|----------------|----------------|----------------|----------------|----------------|
| T1 | T1 | TC20A BDE DIFF | TC21A BDE DIFF | TC22A BDE DIFF | TC23A BDE DIFF |
| TC19A BDE DIFF | TC20A BDE DIFF | TC21A BDE DIFF | TC22A BDE DIFF | TC23A BDE DIFF | |
| 1.9 | 1.5 | 1 | 1 | 1.7 | |
| 2 | 1.2 | 1.2 | 1 | 1.9 | |
| -1.1 | -1.1 | -2 | 1 | -1 | |
| 2.5 | 1.1 | -1.1 | 1 | 1.8 | |
| 2.3 | -1.3 | -1.2 | 1 | 1.1 | |
| 2.6 | 2.3 | -1.4 | 1 | 1.5 | |
| 1.2 | 1 | 1.6 | 1 | 1.5 | |
| 2.1 | 2.1 | -1.4 | 1 | 1.4 | |
| -1.3 | -1.2 | 1.2 | 1 | 1.1 | |
| 1.2 | 1.3 | 1.3 | 1 | 1.2 | |
| 1.6 | 1.1 | 1 | 1 | 1.2 | |
| 1.9 | 1.9 | -1.1 | 1 | 1.4 | |
| 1.5 | -1 | 1.1 | 1 | 1.2 | |
| -1.5 | -1.4 | -1.4 | 1 | -1.2 | |
| 1.7 | 1.3 | -1 | 1 | 1.3 | |
| -1.2 | -1.1 | 1.4 | 1 | 1.4 | |
| -1.2 | -1.1 | 1.5 | 1 | -1.2 | |
| 1.6 | 2.4 | -1.4 | 1 | -1.1 | |
| 2.1 | 1.8 | -1.6 | 1 | 1 | |
| 2 | 2.3 | -1.5 | 1 | 1.3 | |

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TABLE 2 (Page 6)

| normal | Low | G3 | High | G3 |
|----------------|-------------|--------------------------|----------------------|----------------------|
| TC24A BDE DIFF | T1 TC25A | T1+T1S TC28A BDE DIFF | T1 TC29A BDE DIFF | T1 TC30A BDE DIFF |
| -1.1 | 2.9 | 2.1 | 2 | 1.9 |
| 1.4 | 2 | 1.3 | -1.1 | 3.2 |
| -1 | -1.1 | 3.4 | 2.9 | 2.7 |
| -1.1 | 3.2 | -1.4 | 2.5 | 2.3 |
| 2 | 1.3 | -1 | 2.1 | 3 |
| -1.8 | 3.8 | -1.2 | 2.2 | 1.1 |
| 2.2 | 1.1 | 1.6 | 12 | 3 |
| -1.6 | 2.4 | -1.2 | 1.7 | 1.8 |
| 1.4 | -1.3 | 1 | 7.1 | 2.3 |
| 1.6 | 1.5 | 1.4 | 2.5 | 2.3 |
| -1.1 | 2.2 | 3.5 | 2 | 1.8 |
| -1.3 | 2.3 | -1.1 | 1.5 | 1.8 |
| 1.2 | 1.9 | 1.6 | 2.8 | 4.1 |
| 1.4 | -1.3 | 2.1 | 1.8 | 2.4 |
| -1.1 | 2.3 | 1.9 | 1.5 | 1.9 |
| 1.6 | -1.2 | 1.1 | -1 | 3 |
| 1.5 | -2 | 3.6 | 2.2 | 2.4 |
| -1.4 | 1.4 | 3.5 | 1.9 | 1.5 |
| -1.4 | 1.6 | 1.5 | 1.3 | 2.2 |
| -1.9 | 3.2 | -1.3 | 1.6 | -1.2 |

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TABLE 2 (Page 7)

| G1/2 | G2 | G2 | INV | normal |
|----------------|----------------|----------------|----------------|----------------|
| Ta | Ta/T1 | Ta | | |
| TC31A BDE DIFF | TC32A BDE DIFF | TC33A BDE DIFF | TC34A BDE DIFF | TC35A BDE DIFF |
| 1 | 4.4 | 2.5 | 2.3 | 2.3 |
| 1.1 | 9.1 | -1.6 | 1.5 | 1.9 |
| 3.1 | 5.5 | 3.7 | 3.2 | 2.3 |
| 2.7 | 3.5 | 2 | 1.4 | -3.6 |
| 2 | 2 | -2.2 | 1.1 | 1.2 |
| 2.2 | 2.3 | 1.7 | 2.4 | -1.6 |
| 4.2 | 2.5 | -1.5 | 9.8 | 1.1 |
| 1.4 | 3.9 | 1.8 | 3 | 1.2 |
| 3.2 | 2.4 | -1.2 | 6.1 | 1.2 |
| 6.1 | 3.8 | 1.5 | 2.1 | 1.4 |
| 2.4 | 2.7 | 2.4 | 1.9 | 1.8 |
| 1.4 | 3.7 | 1.7 | 2.8 | 1 |
| 5.5 | 2 | 2.4 | 2.2 | 3.1 |
| 2.3 | 3.5 | 2 | 1.9 | 1.7 |
| -1.4 | 3.2 | 2 | 2 | 1.9 |
| 1.2 | 2.2 | 3.4 | 1.3 | 1.5 |
| 3.2 | 4.4 | 3.5 | 2.2 | 3.2 |
| 2.2 | 2.3 | 2.2 | 1.8 | 1.7 |
| 2.4 | 1.3 | 1.4 | 1.6 | 1.8 |
| 1.7 | 1.6 | 1.2 | 1.9 | -1.7 |

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TABLE 2 (Page 8)

| normal | normal | normal | Low | G2/3 |
|----------------|----------------|----------------|----------------------|----------------------|
| TC36A BDE DIFF | TC37A BDE DIFF | TC38A BDE DIFF | Ta TC39A BDE DIFF | T1 TC40A BDE DIFF |
| 1.3 | 1.9 | 1.3 | 2.3 | 1.9 |
| 1.2 | 1.7 | 1.1 | 3 | 3.7 |
| 2.5 | 1.8 | 2.9 | 2.8 | 3.7 |
| -1.2 | -2.3 | -1.6 | 2.4 | 3.2 |
| -1.2 | 1.3 | -1.2 | 6.8 | 1.3 |
| -1.2 | -2 | -1.1 | 2.6 | 1.1 |
| 1.2 | 1.2 | -1.1 | 6 | 4.3 |
| 1.1 | -1.3 | -1 | 3 | 2.1 |
| 1.5 | 1.2 | 1.2 | 4.7 | 4.5 |
| 1.6 | 1.7 | 1.4 | 2.2 | 1.3 |
| -1.4 | -1.9 | 1 | 1.3 | 1.6 |
| 1.1 | -1.1 | -1.1 | 3.1 | 2 |
| 1.9 | 1.8 | 1.6 | 2.5 | 1.6 |
| 1.8 | 1.7 | 1.6 | 3 | 2.9 |
| 1.3 | 1.6 | 1 | 1.7 | 1.6 |
| 1.3 | 1.9 | 1.3 | 2.6 | 1.9 |
| -1.1 | 1 | 1.1 | 1.6 | 2.7 |
| -1.3 | -1.7 | -1 | 1.4 | 1.6 |
| 1.3 | 2.3 | 1.2 | 3.3 | 2.8 |
| -1.4 | -2.1 | -1.4 | 1.9 | -1 |

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TABLE 2 (Page 9)

| G2 | G2 | G2 | G2 | INV |
|----------------|----------------|----------------|----------------|----------------|
| Ta | Ta | T1 | Ta | |
| TC41A BDE DIFF | TC42A BDE DIFF | TC43A BDE DIFF | TC44A BDE DIFF | TC45A BDE DIFF |
| 1.9 | 2.1 | 2.3 | 2.3 | 2.4 |
| 2.4 | 2.2 | 4.6 | 3.5 | 1.2 |
| 3.7 | 3.3 | 3.4 | 3.6 | 3.4 |
| 1.2 | 2.1 | 1.9 | 3.2 | -1.8 |
| 1 | 2.3 | 5 | 2 | 1.1 |
| 1.9 | 1.9 | 1.2 | 3.2 | 1.3 |
| 1.5 | 1.3 | 7 | 11 | 1.3 |
| 1.5 | 1.4 | 1.7 | 3.1 | 1.2 |
| -1.1 | 1.1 | 4.7 | 6.7 | 1.1 |
| 2.6 | 2.2 | 2.7 | 2 | 1.7 |
| 2.3 | 1.6 | 1.9 | 2.8 | 1.2 |
| 1.5 | 1.6 | 1.8 | 2.5 | 1.2 |
| 1.7 | 2.1 | 2 | 2.1 | 2 |
| 2.6 | 2.1 | 2.4 | 2.8 | 1.5 |
| 1.4 | 1.6 | 1.6 | 2 | 2 |
| 3.1 | 1.4 | 2.6 | 2.8 | 1.3 |
| 3.1 | 2.3 | 1.6 | 1.4 | 2 |
| 2.1 | 1.6 | 1.8 | 2.9 | 1.2 |
| 2.5 | 1.9 | 1.4 | 2.3 | 1.6 |
| 1.5 | 1.3 | 1 | 2.6 | 1.3 |

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TABLE 2 (Page 10)

| normal | normal | normal | |
|----------------|----------------|----------------|-------|
| TC46A BDE DIFF | TC47A BDE DIFF | TC48A BDE DIFF | sectd |
| 1 | 1 | -1.1 | -1.8 |
| -1.2 | 1 | -1.1 | |
| 1.7 | 1 | 3.6 | 1.1 |
| -1.4 | 1 | -1.1 | -1.2 |
| -1.2 | 1 | 1.1 | |
| 1 | 1 | -1.3 | -1.6 |
| -1 | 1 | 1.1 | 1.3 |
| -1.1 | 1 | -1.2 | -1.9 |
| 1.1 | 1 | -1 | 1.9 |
| 1 | 1 | 1.1 | -2.2 |
| -1 | 1 | -1.2 | -2.2 |
| -1.2 | 1 | -1.3 | -1.6 |
| 1 | 1 | 1.1 | -1.2 |
| 1.1 | 1 | 1.4 | |
| -1.1 | 1 | -1.3 | -1.9 |
| 1 | 1 | -1 | |
| 1 | 1 | 1.1 | 3.6 |
| -1.1 | 1 | -1.2 | -2.3 |
| -1.1 | 1 | -1.5 | |
| -1.1 | 1 | -1.3 | -1.8 |

Please renumber pages 89 to 104 of the specification as pages 106 to 121.

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REMARKS

In a March 2, 2005 telephone conference between Examiner Johannsen and Daniel N. Smith of the undersigned's office, Examiner Johannsen requested certain amendments to the specification of the above-identified application. Specifically, Examiner Johannsen requested that pages 56 to 58 of the specification be submitted as figures and that the tables on pages 83 to 88 be replaced with more legible versions.

In response, applicants attach hereto as Exhibit A six (6) sheets of new Figures 1-6.

Further, applicants have amended the specification to include a Brief Description of Figures section with a description of each of the figures; have deleted pages 56 to 58; and have amended pages 55 and 59 to refer to Figures 1-6. Applicants maintain that the above amendments do not create any issue of new matter and are supported, *inter alia*, on pages 55 to 59 of the application as filed.

Applicants have also amended the specification to include larger replacement tables for the tables on pages 83 to 88. Applicants maintain that these amendments also do not create any issue of new matter and are supported, *inter alia*, on pages 83 to 88 of the application as filed.

In conclusion, based on the preceding amendments to specification requested by the Examiner and the remarks, applicants respectfully request prompt issuance of the subject application for which the issue fee was paid on December 15, 2004.

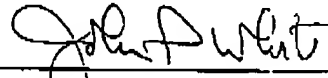
If a telephone interview would be of assistance in advancing issuance of the subject application, applicants' undersigned attorney invites the Examiner to telephone him at the number

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provided below.

No fee is deemed necessary in connection with the filing of this Amendment. However, if any other fee is required, authorization is hereby given to charge the amount of such fee to Deposit Account No. 03-3125.

Respectfully submitted,



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